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**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/572,027**

TEAM 4

DATE: 02/14/96
TIME: 17:56:58

INPUT SET: S8732.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/572,027DATE: 02/14/96
TIME: 17:57:01

INPUT SET: S8732.raw

47 (C) CLASSIFICATION:
48
49 (viii) ATTORNEY/AGENT INFORMATION:
50 (A) NAME: Ellinger, Mark S.
51 (B) REGISTRATION NUMBER: 34,812
52 (C) REFERENCE/DOCKET NUMBER: A21-535.10
53
54 (ix) TELECOMMUNICATION INFORMATION:
55 (A) TELEPHONE: 612/335-5070
56 (B) TELEFAX: 612/288-9696
57
58 (2) INFORMATION FOR SEQ ID NO:1:
59
60 (i) SEQUENCE CHARACTERISTICS:
61 (A) LENGTH: 1155 base pairs
62 (B) TYPE: nucleic acid
63 (C) STRANDEDNESS: single
64 (D) TOPOLOGY: linear
65
66 (ii) MOLECULE TYPE: DNA
67
68 (iii) HYPOTHETICAL: NO
69
70 (iv) ANTI-SENSE: NO
71
72 (vi) ORIGINAL SOURCE:
73 (A) ORGANISM: Brassica napus
74
75 (ix) FEATURE:
76 (D) OTHER INFORMATION: Wild type D form.
77
78
79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
80
81 ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT 48
82 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
83 1 5 10 15
84
85 GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT 96
86 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
87 20 25 30
88
89 GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG 144
90 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
91 35 40 45
92
93 ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC 192
94 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
95 50 55 60
96
97 TGC TTC TAC TAC NTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT 240
98 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
99 65 70 75 80

RAW SEQUENCE LISTING
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100	CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAA GGG TGC GTC	288
101	Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
102	85 90 95	
104	CTA ACC GGC GTC TGG GTC ATA GCC CAC GAA TGC GGC CAC CAC GCC TTC	336
105	Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
106	100 105 110	
108	AGC GAC TAC CAG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC	384
109	Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
110	115 120 125	
112	TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC	432
113	Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His	
114	130 135 140	
116	CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG	480
117	His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
118	145 150 155 160	
120	AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG	528
121	Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
122	165 170 175	
124	GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG	576
125	Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
126	180 185 190	
128	TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC TTC CGT	624
129	Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg	
130	195 200 205	
132	TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC	672
133	Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
134	210 215 220	
136	CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TAC GGT CTC	720
137	Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
138	225 230 235 240	
140	TTC CGT TAC GCC GCC GGC CAG GGA GTG GCC TCG ATG GTC TGC TTC TAC	768
141	Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
142	245 250 255	
144	GGA GTC CCG CTT CTG ATT GTC AAT GGT TTC CTC GTG TTG ATC ACT TAC	816
145	Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
146	260 265 270	
148	TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAC GAT TCG TCC GAG TGG	864
149	Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
150	275 280 285	
152		

RAW SEQUENCE LISTING
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153 GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC 912
154 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
155 290 295 300
156
157 TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT 960
158 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
159 305 310 315 320
160
161 CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG 1008
162 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
163 325 330 335
164
165 ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG 1056
166 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
167 340 345 350
168
169 GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG 1104
170 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
171 355 360 365
172
173 GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T 1153
174 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
175 370 375 380
176
177 GA 1155
178
179
180 (2) INFORMATION FOR SEQ ID NO:2:
181
182 (i) SEQUENCE CHARACTERISTICS:
183 (A) LENGTH: 384 amino acids
184 (B) TYPE: amino acid
185 (D) TOPOLOGY: linear
186
187 (ii) MOLECULE TYPE: protein
188
189 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
190
191 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
192 1 5 10 15
193
194 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
195 20 25 30
196
197 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
198 35 40 45
199
200 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
201 50 55 60
202
203 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
204 65 70 75 80
205

RAW SEQUENCE LISTING
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206 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
207 85 90 95
208
209 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
210 100 105 110
211
212 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
213 115 120 125
214
215 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
216 130 135 140
217
218 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
219 145 150 155 160
220
221 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
222 165 170 175
223
224 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
225 180 185 190
226
227 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
228 195 200 205
229
230 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
231 210 215 220
232
233 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
234 225 230 235 240
235
236 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
237 245 250 255
238
239 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
240 260 265 270
241
242 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
243 275 280 285
244
245 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
246 290 295 300
247
248 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
249 305 310 315 320
250
251 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
252 325 330 335
253
254 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
255 340 345 350
256
257 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
258 355 360 365

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SEQUENCE VERIFICATION REPORT
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Original Text